

GenCore version 5.1.6
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OM protein - protein search, using sw model
 Run on: December 26, 2004, 16:59:06 ; Search time 12.1928 Seconds
 (without alignments)
 1996.498 Million cell updates/sec

Title: US-10-655-873-8
 Perfect score: 1304
 Sequence: 1 MWPPGSASQQPPSPAAATGL.....HAFRIRAVTIDRVMSYLNAS 253
 Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing First 45 summaries

Database : PIR79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	1304	100.0	253	2	B38957		interleukin 12A precursor [validated] - human
2	644	49.4	215	2	156135		N;Alternate names: Cytotoxic lymphocyte maturation factor 35K chain; natural killer cell C;Species: Homo sapiens (man)
3	98.5	7.6	438	2	T45785		C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
4	97	7.4	1301	2	T07321		C;Accession: B38957; A39359; A36055
5	93.5	7.2	1489	2	G83771		R;Wolf, S.P.; Temple, P.A.; Kobayashi, M.; Young, D.; Dicig, M.; Lowe, L.; Dzialo, R.; i, G.; Perussia, B.
6	91	7.0	661	2	T08872		J. Immunol. 146, 3074-3081, 1991
7	91	7.0	729	1	A34796		A;Title: Cloning of cDNA for natural killer cell stimulatory factor, a heterodimeric cy
8	90.5	6.9	781	1	TVFFDF		A;Reference number: A38957; MUID:91201875; PMID:90370873; PMID:1673147
9	90	6.9	349	2	D70398		A;Accession: B38957
10	89.5	6.9	680	2	T04647		A;Molecule type: mRNA
11	89.5	6.9	1040	2	AH1926		A;Residues: 35-246, 'T', 248-253 <GUB>
12	89	6.8	586	2	JC4778		A;Cross-references: GB:M65271; PIDN:AAA35694.1; PID:9180623; R;Gubler, U.; Chua, A.O.; Schoenhaut, D.S.; Dwyer, C.M.; McComas, W.; Motyka, R.; Nabav
13	88.5	6.8	1111	2	T01078		Proc. Natl. Acad. Sci. U.S.A. 88, 4143-4147, 1991
14	87	6.7	1445	2	T50508		A;Title: Coexpression of two distinct genes is required to generate secreted bioactive
15	86	6.6	407	2	F72343		A;Reference number: A36055; MUID:90370873; PMID:2204066
16	86	6.6	830	1	B44047		A;Accession: A36055
17	86	6.6	830	2	T44186		A;Status: preliminary
18	86	6.6	830	2	T43999		A;Molecule type: protein
19	85.5	6.6	868	2	T25716		A;Residues: 'X', 58-70, 'X', 72-82 <STE>
20	85.5	6.6	950	2	T38777		C;Genetics:
21	85.5	6.6	1121	2	T25715		A;Gene: GDB:IL12A; NKSF1
22	85	6.5	930	2	T32017		A;Cross-references: GDB:127869; OMIM:161560
23	85	6.5	4385	2	T29042		A;Map position: 3p12-3q13.2
24	84	6.4	3968	2	A44265		C;Keywords: cytokine; glycoprotein; heterodimer
25	83.5	6.4	630	2	A49656		F:57-253/Product: interleukin 12A #status predicted <MAT> (covalent) carbohydrate (Asn) (covalent) #status predicted
26	83.5	6.4	816	2	D84601		Query Match 100.0%; Score 1304; DB 2; Length 253;
27	83	6.4	287	2	T48548		Best Local Similarity 100.0%; Pred. No. 3.5e-101;
28	83	6.4	830	1	A44047		Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
29	83	6.4	1698	2	S51869		1 MWPPGSASQQPPSPAAATGLHPARPVSLQCRLSMCPARSLLLVATLVLDDHLSLARNLP 60
							1 MWPPGSASQQPPSPAAATGLHPARPVSLQCRLSMCPARSLLLVATLVLDDHLSLARNLP 60

Db	61	VATPPGMFPCLHHSQNLLRAVSNMLQKARQTLLEFYPCTSEEIDHEDITKDRTSTVEACL	120	Best Local Similarity 25.6%; Pred. No. 1.5; Matches 42; Conservative 27; Mismatches 48; Indels 47; Gaps 9;
Qy	121	PLELTKNESCLNSRETSFITNGSCLASRKTSFMMALCLSSIYEDLKMYQVEFKTMNAKLL	180	C;Species: Mus musculus (house mouse) C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
Db	121	PLELTKNESCLNSRETSFITNGSCLASRKTSFMMALCLSSIYEDLKMYQVEFKTMNAKLL	180	C;Accession: I56135 C;Text_Change: 09-Jul-2004 C;Sequence_Revision: 14-May-1999 #text_change 09-Jul-2004
Qy	181	MDPKRQIFLDQNMFLAVIDELMQALNFNSETVPQKSSLEEPDFYKTKRKLICILLHAFRIRA	240	R;Schoenhaut, D.S.; Chua, A.O.; Wolitzky, A.G.; Quinn, P.M.; Dwyer, C.M.; Gately, M.K.; J. Immunol. 148, 3433-3440, 1992
Db	181	MDPKRQIFLDQNMFLAVIDELMQALNFNSETVPQKSSLEEPDFYKTKRKLICILLHAFRIRA	240	A;Title: Cloning and Expression of Murine IL-12. A;Reference number: 156135; PMID:92268481; PMID:1350290
Qy	241	VTIDRVMVSYLNAS 253		A;Accession: I56135 A;Status: preliminary; translated from GB/EMBL/DBJ A;Molecule type: mRNA A;Residues: 1-215 <RES> A;Cross-references: UNIPROT:P43431; GB:MB86672; NID:9198336; PIDN:AAA39292.1; PID:9198337
Db	241	VTIDRVMVSYLNAS 253		Query Match Score 64.4; DB 2; Length 215; Best Local Similarity 58.9%; Pred. No. 2.5e-46; Matches 129; Conservative 33; Mismatches 53; Indels 4; Gaps 1;
Qy	156135	interleukin 12 p35 subunit - mouse		Query Match Score 64.4; DB 2; Length 215; Best Local Similarity 58.9%; Pred. No. 2.5e-46; Matches 129; Conservative 33; Mismatches 53; Indels 4; Gaps 1;
Db		C;Species: Mus musculus (house mouse) C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004		Query Match Score 64.4; DB 2; Length 215; Best Local Similarity 58.9%; Pred. No. 2.5e-46; Matches 129; Conservative 33; Mismatches 53; Indels 4; Gaps 1;
Qy		C;Accession: I56135 C;Text_Change: 09-Jul-2004 C;Sequence_Revision: 14-May-1999 #text_change 09-Jul-2004		Query Match Score 64.4; DB 2; Length 215; Best Local Similarity 58.9%; Pred. No. 2.5e-46; Matches 129; Conservative 33; Mismatches 53; Indels 4; Gaps 1;
Db		R;Wakasugi, T.; Nagai, T.; Kapoor, M.; Ito, M.; Sugita, M.; Ito, S.; Tsudzuki, J.; Proc. Natl. Acad. Sci. U.S.A. 94, 5967-5972, 1997		Query Match Score 64.4; DB 2; Length 215; Best Local Similarity 58.9%; Pred. No. 2.5e-46; Matches 129; Conservative 33; Mismatches 53; Indels 4; Gaps 1;
Qy		A;Title: Complete nucleotide sequence of the chloroplast genome from the green alga Chlamydomonas reinhardtii. A;Reference number: 215985; PMID:97303241; PMID:9159184		Query Match Score 64.4; DB 2; Length 215; Best Local Similarity 58.9%; Pred. No. 2.5e-46; Matches 129; Conservative 33; Mismatches 53; Indels 4; Gaps 1;
Db		A;Accession: T07321 A;Status: preliminary; translated from GB/EMBL/DBJ A;Molecule type: DNA A;Residues: 1-1301 <WAK> A;Cross-references: UNIPROT:P56299; EMBL:AB001684; NID:92224352; PIDN:BAAS57969.1; PID:9159184		Query Match Score 64.4; DB 2; Length 215; Best Local Similarity 58.9%; Pred. No. 2.5e-46; Matches 129; Conservative 33; Mismatches 53; Indels 4; Gaps 1;
Qy		C;Genetics: A;Gene: rpoB A;Genome: chloroplast C;Superfamily: DNA-directed RNA polymerase beta chain C;Keywords: chloroplast; nucleotidyltransferase C;Cross-references: UNIPROT:P56299; EMBL:AB001684; NID:92224352; PIDN:BAAS57969.1; PID:9159184		Query Match Score 64.4; DB 2; Length 215; Best Local Similarity 58.9%; Pred. No. 2.5e-46; Matches 129; Conservative 33; Mismatches 53; Indels 4; Gaps 1;
Db		A;Molecule type: DNA A;Residues: 1-1301 <WAK> A;Cross-references: UNIPROT:P56299; EMBL:AB001684; NID:92224352; PIDN:BAAS57969.1; PID:9159184		Query Match Score 64.4; DB 2; Length 215; Best Local Similarity 58.9%; Pred. No. 2.5e-46; Matches 129; Conservative 33; Mismatches 53; Indels 4; Gaps 1;
Qy		RESULT 2		Query Match Score 64.4; DB 2; Length 215; Best Local Similarity 58.9%; Pred. No. 2.5e-46; Matches 129; Conservative 33; Mismatches 53; Indels 4; Gaps 1;
Db		interleukin 12 p35 subunit - mouse		Query Match Score 64.4; DB 2; Length 215; Best Local Similarity 58.9%; Pred. No. 2.5e-46; Matches 129; Conservative 33; Mismatches 53; Indels 4; Gaps 1;
Qy		C;Species: Mus musculus (house mouse) C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004		Query Match Score 64.4; DB 2; Length 215; Best Local Similarity 58.9%; Pred. No. 2.5e-46; Matches 129; Conservative 33; Mismatches 53; Indels 4; Gaps 1;
Db		C;Accession: I56135 C;Text_Change: 09-Jul-2004 C;Sequence_Revision: 14-May-1999 #text_change 09-Jul-2004		Query Match Score 64.4; DB 2; Length 215; Best Local Similarity 58.9%; Pred. No. 2.5e-46; Matches 129; Conservative 33; Mismatches 53; Indels 4; Gaps 1;
Qy		R;Delenby, M.; Berger, C.; Cooke, R.; Grellet, F.; Laudie, M.; Mewes, H.W.; Lemcke, K.; Submitted to the Protein Sequence Database, December 1999		Query Match Score 64.4; DB 2; Length 215; Best Local Similarity 58.9%; Pred. No. 2.5e-46; Matches 129; Conservative 33; Mismatches 53; Indels 4; Gaps 1;
Db		A;Reference number: Z23013 A;Accession: T45785 A;Status: preliminary		Query Match Score 64.4; DB 2; Length 215; Best Local Similarity 58.9%; Pred. No. 2.5e-46; Matches 129; Conservative 33; Mismatches 53; Indels 4; Gaps 1;
Qy		RESULT 3		Query Match Score 64.4; DB 2; Length 215; Best Local Similarity 58.9%; Pred. No. 2.5e-46; Matches 129; Conservative 33; Mismatches 53; Indels 4; Gaps 1;
Db		T45785 hypothetical protein F26013.180 - Arabidopsis thaliana		Query Match Score 64.4; DB 2; Length 215; Best Local Similarity 58.9%; Pred. No. 2.5e-46; Matches 129; Conservative 33; Mismatches 53; Indels 4; Gaps 1;
Qy		C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004		Query Match Score 64.4; DB 2; Length 215; Best Local Similarity 58.9%; Pred. No. 2.5e-46; Matches 129; Conservative 33; Mismatches 53; Indels 4; Gaps 1;
Db		C;Accession: T45785 R;Delenby, M.; Berger, C.; Cooke, R.; Grellet, F.; Laudie, M.; Mewes, H.W.; Lemcke, K.; Submitted to the Protein Sequence Database, December 1999		Query Match Score 64.4; DB 2; Length 215; Best Local Similarity 58.9%; Pred. No. 2.5e-46; Matches 129; Conservative 33; Mismatches 53; Indels 4; Gaps 1;
Qy		A;Reference number: Z23013 A;Accession: T45785 A;Status: preliminary		Query Match Score 64.4; DB 2; Length 215; Best Local Similarity 58.9%; Pred. No. 2.5e-46; Matches 129; Conservative 33; Mismatches 53; Indels 4; Gaps 1;
Db		RESULT 4		Query Match Score 64.4; DB 2; Length 215; Best Local Similarity 58.9%; Pred. No. 2.5e-46; Matches 129; Conservative 33; Mismatches 53; Indels 4; Gaps 1;
Qy		T07321 DNA-directed RNA polymerase (EC 2.7.7.6) beta chain - Chlorella vulgaris chloroplast		Query Match Score 64.4; DB 2; Length 215; Best Local Similarity 58.9%; Pred. No. 2.5e-46; Matches 129; Conservative 33; Mismatches 53; Indels 4; Gaps 1;
Db		C;Species: Chlorella vulgaris C;Text_Change: 09-Jul-2004 C;Sequence_Revision: 14-May-1999 #text_change 09-Jul-2004		Query Match Score 64.4; DB 2; Length 215; Best Local Similarity 58.9%; Pred. No. 2.5e-46; Matches 129; Conservative 33; Mismatches 53; Indels 4; Gaps 1;
Qy		R;Wakasugi, T.; Nagai, T.; Kapoor, M.; Sugita, M.; Ito, M.; Ito, S.; Tsudzuki, J.; Proc. Natl. Acad. Sci. U.S.A. 94, 5967-5972, 1997		Query Match Score 64.4; DB 2; Length 215; Best Local Similarity 58.9%; Pred. No. 2.5e-46; Matches 129; Conservative 33; Mismatches 53; Indels 4; Gaps 1;
Db		A;Title: Complete nucleotide sequence of the chloroplast genome from the green alga Chlamydomonas reinhardtii. A;Reference number: 215985; PMID:97303241; PMID:9159184		Query Match Score 64.4; DB 2; Length 215; Best Local Similarity 58.9%; Pred. No. 2.5e-46; Matches 129; Conservative 33; Mismatches 53; Indels 4; Gaps 1;
Qy		A;Accession: T07321 A;Status: preliminary		Query Match Score 64.4; DB 2; Length 215; Best Local Similarity 58.9%; Pred. No. 2.5e-46; Matches 129; Conservative 33; Mismatches 53; Indels 4; Gaps 1;
Db		RESULT 5		Query Match Score 64.4; DB 2; Length 215; Best Local Similarity 58.9%; Pred. No. 2.5e-46; Matches 129; Conservative 33; Mismatches 53; Indels 4; Gaps 1;
Qy		G83771 hypothetical protein BH0975 [Imported] - Bacillus halodurans (strain C-125)		Query Match Score 64.4; DB 2; Length 215; Best Local Similarity 58.9%; Pred. No. 2.5e-46; Matches 129; Conservative 33; Mismatches 53; Indels 4; Gaps 1;
Db		C;Species: Bacillus halodurans C;Text_Change: 09-Jul-2004 C;Sequence_Revision: 01-Dec-2000 #text_change 09-Jul-2004		Query Match Score 64.4; DB 2; Length 215; Best Local Similarity 58.9%; Pred. No. 2.5e-46; Matches 129; Conservative 33; Mismatches 53; Indels 4; Gaps 1;
Qy		R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; H. Nucleic Acids Res. 28, 4317-4331, 2000		Query Match Score 64.4; DB 2; Length 215; Best Local Similarity 58.9%; Pred. No. 2.5e-46; Matches 129; Conservative 33; Mismatches 53; Indels 4; Gaps 1;
Db		A;Title: Complete genome sequence of the alkaliiphilic bacterium Bacillus halodurans		Query Match Score 64.4; DB 2; Length 215; Best Local Similarity 58.9%; Pred. No. 2.5e-46; Matches 129; Conservative 33; Mismatches 53; Indels 4; Gaps 1;
Qy		A;Reference number: A83650; PMID:20512582; G83771		Query Match Score 64.4; DB 2; Length 215; Best Local Similarity 58.9%; Pred. No. 2.5e-46; Matches 129; Conservative 33; Mismatches 53; Indels 4; Gaps 1;

KW Human; interleukin 12; IL-12; heterodimeric complex; immunogenic;
 KW Leishmania; antigen; leishmaniasis; cell-mediated immunity; adjuvant;
 KW TH1 helper cell; TH2 helper cell; alum; cytokine; bacterium; cancer;
 KW vaccine; cell surface; membrane; glycoprotein; antigen presenting cell.

XX Homo sapiens.

XX PN US5571515-A.

XX PD 05-NOV-1996.

XX PF 17-JUN-1994; 94US-00265087.

XX PR 18-APR-1994; 94US-00229282.

PA (WIST-) WISTAR INST ANATOMY & BIOLOGY.
 PA (UYPE-) UNIV PENNSYLVANIA.

PI Trinchieri G, Scott P;

XX DR WPI; 1996-505347/50.

XX DR N-PSDB; AAT48098.

PT Immunogenic compn. to improve cell mediated immune response - contains
 PT soluble leishmania antigen and interleukin-12 as adjuvant.

PS Disclosure; Col 17-22; 22pp; English.

CC This is the amino acid sequence of the human interleukin (IL)-12 40 kD
 CC subunit. IL-12 is a heterodimeric complex composed of the 40 kD subunit
 CC and a 30 kD subunit (AAW07399). The complex is used in a novel
 CC immunogenic composition comprising a soluble Leishmania antigen with IL-
 CC 12, for protection against leishmaniasis. The addition of IL-12 improves
 CC cell-mediated immunity by inducing TH1 helper cells (as opposed to TH2
 CC cells which are induced by alum adjuvant) and does not cause uncontrolled
 CC release of other cytokines (in contrast to bacterial adjuvants). IL-12
 CC can also be used as a cancer vaccine by association with the protein B7,
 CC a soluble, cell-surface (membrane)-bound glycoprotein which is expressed
 CC in antigen presenting cells. (Updated on 25-MAR-2003 to correct PP
 CC field.)

XX SQ Sequence 328 AA;

Query Match 100.0%; Score 1758; DB 2; Length 328;
 Best Local Similarity 100.0%; Pred. No. 1.5e-148;
 Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MCHQQLVISWFSVLFLASPLVIAIWELLKKDQVYVVBLDWYPDAPGEMVVLTCDTPEEDGITW 60
 Db 1 MCHQQLVISWFSVLFLASPLVIAIWELLKKDQVYVVBLDWYPDAPGEMVVLTCDTPEEDGITW 60
 Qy 61 TLDQSSSEVVLGSGKTLTIVQVKBFGDAGQTCHKGGEVTLHSLLLHKKEDGIVSTDILKDQ 120
 Db 61 TLDQSSSEVVLGSGKTLTIVQVKFGDAGQTCHKGGEVTLHSLLLHKKEDGIVSTDILKDQ 120
 Qy 121 KEPKQKTKPLRCEAKNYSGRFTCWWLIT1STDLTFSVKSRRGSSDPOGVTCGAATLSAERV 180
 Db 121 KEPKQKTKPLRCEAKNYSGRFTCWWLIT1STDLTFSVKSRRGSSDPOGVTCGAATLSAERV 180

Qy 181 RGDNKKEYYSVCEQDSDACPAAEESLPIEVMDAVHKLKYENTYSSFFIRDIIKPDPPKN 240
 Db 181 RGDNKKEYYSVCEQDSDACPAAEESLPIEVMDAVHKLKYENTYSSFFIRDIIKPDPPKN 240
 Qy 241 LQLKPLKNSRQVEVSWEYPTPHSYFYSLTFCVQVQGKSKREKKDRVFTDKTSATVIC 300
 Db 241 LQLKPLKNSRQVEVSWEYPTPHSYFYSLTFCVQVQGKSKREKKDRVFTDKTSATVIC 300

Qy 301 RKNASISVRAQDRYSSSSWSENAVPCS 328
 Db 301 RKNASISVRAQDRYSSSSWSENAVPCS 328

RESULT 4

AAW24235
 ID AAW24235 standard; protein; 328 AA.
 XX
 AC AAW24235;
 XX
 DE 40 kDa subunit of human cytotoxic lymphocyte maturation factor.

XX
 KW Cytotoxic lymphocyte maturation factor; CLMF; 40 kDa subunit;

XX KW interleukin-2; T-cell growth; antibody; lymphokine activated killer cell;

XX KW CLMF bioactivity inhibition; affinity ligand; transplantation;

XX KW cytotoxic T cell proliferation.

XX OS Homo sapiens.

XX PN EP790255-A2.

XX PD 20-AUG-1997.

XX PF 09-DEC-1990; 97EP-00104656.

XX PR 22-DEC-1989; 89US-00455708.

XX PR 09-MAY-1990; 90US-00520935.

XX PR 27-AUG-1990; 90US-00572284.

XX PR 09-DEC-1990; 90EP-00123670.

XX PA (HOFFMANN LA ROCHE & CO AG F.

XX PA (HOFFMANN LA ROCHE & CO AG F.

XX PI Chizzonite RA, Gately MK, Gubler UA, Hulmes JD, Pan YE;

XX PI Podlanski FJ, Stern AS;

XX DR WPI; 1997-404698/38.

XX DR N-PSDB; AAT77849.

XX PA Antibodies to cytotoxic lymphocyte maturation factor protein - useful as

XX PT affinity ligands, assay reagents and medicaments.

XX PS Claim 2; Fig 25; 80pp; English.

XX PS Sequence 328 AA;

CC The present sequence represents the 40 kDa subunit of cytotoxic
 CC lymphocyte maturation factor (CLMF) protein. The natural CLMF protein is
 CC a 75 kDa heterodimer, where the 2 subunits (see AAW24236 for the 35 kDa
 CC subunit) are bonded together via one or more disulphide bonds. CLMF
 CC protein is produced by a human B lymphoblastoid cell line. CLMF
 CC synergistically induces, in the presence of interleukin-2, the cytolytic
 CC activity of lymphokine activated killer cells. CLMF is also capable of
 CC stimulating T-cell growth. A novel antibody directed against an epitope
 CC of CLMF protein (see AAW24237 for epitope) is capable of neutralising
 CC and/or inhibiting CLMF bioactivity. This antibody may be used as an
 CC affinity ligand for purifying the CLMF protein. The antibody can also be
 CC used as an assay reagent for detecting the CLMF protein, and as a
 CC medicament for selectively blocking the proliferation and activation of
 CC cytotoxic T cells, e.g. in transplantation, e.g. in transplantation and activation of
 CC cytotoxic T cell proliferation. (Updated on 25-MAR-2003 to correct PR field.)

XX SQ Sequence 328 AA;

CC The present sequence represents the 40 kDa subunit of cytotoxic
 CC lymphocyte maturation factor (CLMF) protein. The natural CLMF protein is
 CC a 75 kDa heterodimer, where the 2 subunits (see AAW24236 for the 35 kDa
 CC subunit) are bonded together via one or more disulphide bonds. CLMF
 CC protein is produced by a human B lymphoblastoid cell line. CLMF
 CC synergistically induces, in the presence of interleukin-2, the cytolytic
 CC activity of lymphokine activated killer cells. CLMF is also capable of
 CC stimulating T-cell growth. A novel antibody directed against an epitope
 CC of CLMF protein (see AAW24237 for epitope) is capable of neutralising
 CC and/or inhibiting CLMF bioactivity. This antibody may be used as an
 CC affinity ligand for purifying the CLMF protein. The antibody can also be
 CC used as an assay reagent for detecting the CLMF protein, and as a
 CC medicament for selectively blocking the proliferation and activation of
 CC cytotoxic T cells, e.g. in transplantation, e.g. in transplantation and activation of
 CC cytotoxic T cell proliferation. (Updated on 25-MAR-2003 to correct PR field.)

XX SQ Sequence 328 AA;

CC The present sequence represents the 40 kDa subunit of cytotoxic

CC lymphocyte maturation factor (CLMF) protein. The natural CLMF protein is
 CC a 75 kDa heterodimer, where the 2 subunits (see AAW24236 for the 35 kDa
 CC subunit) are bonded together via one or more disulphide bonds. CLMF
 CC protein is produced by a human B lymphoblastoid cell line. CLMF
 CC synergistically induces, in the presence of interleukin-2, the cytolytic
 CC activity of lymphokine activated killer cells. CLMF is also capable of
 CC stimulating T-cell growth. A novel antibody directed against an epitope
 CC of CLMF protein (see AAW24237 for epitope) is capable of neutralising
 CC and/or inhibiting CLMF bioactivity. This antibody may be used as an
 CC affinity ligand for purifying the CLMF protein. The antibody can also be
 CC used as an assay reagent for detecting the CLMF protein, and as a
 CC medicament for selectively blocking the proliferation and activation of
 CC cytotoxic T cells, e.g. in transplantation, e.g. in transplantation and activation of
 CC cytotoxic T cell proliferation. (Updated on 25-MAR-2003 to correct PR field.)

CC Sequence 328 AA;

Qy 1 MCHQQLVISWFSVLFLASPLVIAIWELLKKDQVYVVBLDWYPDAPGEMVVLTCDTPEEDGITW 60
 Db 1 MCHQQLVISWFSVLFLASPLVIAIWELLKKDQVYVVBLDWYPDAPGEMVVLTCDTPEEDGITW 60
 Qy 61 TLDQSSSEVVLGSGKTLTIVQVKBFGDAGQTCHKGGEVTLHSLLLHKKEDGIVSTDILKDQ 120
 Db 61 TLDQSSSEVVLGSGKTLTIVQVKFGDAGQTCHKGGEVTLHSLLLHKKEDGIVSTDILKDQ 120
 Qy 121 KEPKQKTKPLRCEAKNYSGRFTCWWLIT1STDLTFSVKSRRGSSDPOGVTCGAATLSAERV 180
 Db 121 KEPKQKTKPLRCEAKNYSGRFTCWWLIT1STDLTFSVKSRRGSSDPOGVTCGAATLSAERV 180

Qy 181 RGDNKKEYYSVCEQDSDACPAAEESLPIEVMDAVHKLKYENTYSSFFIRDIIKPDPPKN 240
 Db 181 RGDNKKEYYSVCEQDSDACPAAEESLPIEVMDAVHKLKYENTYSSFFIRDIIKPDPPKN 240
 Qy 241 LQLKPLKNSRQVEVSWEYPTPHSYFYSLTFCVQVQGKSKREKKDRVFTDKTSATVIC 300
 Db 241 LQLKPLKNSRQVEVSWEYPTPHSYFYSLTFCVQVQGKSKREKKDRVFTDKTSATVIC 300

Qy 301 RKNASISVRAQDRYSSSSWSENAVPCS 328
 Db 301 RKNASISVRAQDRYSSSSWSENAVPCS 328

Qy 121 KEPKQKTKPLRCEAKNYSGRFTCWWLIT1STDLTFSVKSRRGSSDPOGVTCGAATLSAERV 180

Query Match 100.0%; Score 1758; DB 2; Length 328;
 Best Local Similarity 100.0%; Pred. No. 1.5e-148;
 Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MCHQQLVISWFSVLFLASPLVIAIWELLKKDQVYVVBLDWYPDAPGEMVVLTCDTPEEDGITW 60
 Db 1 MCHQQLVISWFSVLFLASPLVIAIWELLKKDQVYVVBLDWYPDAPGEMVVLTCDTPEEDGITW 60
 Qy 61 TLDQSSSEVVLGSGKTLTIVQVKBFGDAGQTCHKGGEVTLHSLLLHKKEDGIVSTDILKDQ 120
 Db 61 TLDQSSSEVVLGSGKTLTIVQVKFGDAGQTCHKGGEVTLHSLLLHKKEDGIVSTDILKDQ 120
 Qy 121 KEPKQKTKPLRCEAKNYSGRFTCWWLIT1STDLTFSVKSRRGSSDPOGVTCGAATLSAERV 180
 Db 121 KEPKQKTKPLRCEAKNYSGRFTCWWLIT1STDLTFSVKSRRGSSDPOGVTCGAATLSAERV 180

Qy 121 KEPKQKTKPLRCEAKNYSGRFTCWWLIT1STDLTFSVKSRRGSSDPOGVTCGAATLSAERV 180

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OM nucleic - nucleic search, using bw model

Run on: December 26, 2004, 09:32:55 ; Search time 437.322 seconds
 (without alignments)
 15189.855 Million cell updates/sec

Title: US-10-655-873-11

Perfect score: 1193

Sequence: taaaggatcgtttagaag.....taaaggatcgttccaaact 1193

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 4105333 seqs, 2784095677 residues

Total number of hits satisfying chosen parameters: 8210666

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published_Applications_NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/PCR_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/PCRTUS_PUBCOMB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*

8: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*

11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*

12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*

13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*

16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*

17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*

18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*

19: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*

20: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1193	100.0	1193	15	US-10-284-740-13
2	1193	100.0	1193	16	US-10-641-643-1302
3	1193	100.0	1193	17	US-10-283-975A-258
4	1193	100.0	1193	17	US-10-654-796-6
5	1193	100.0	1193	17	US-10-654-763-6
6	1193	100.0	1193	18	US-10-733-878-280
7	963.2	80.7	987	10	US-09-882-945A-141
8	963.2	80.7	987	18	US-10-807-114-141
9	718.8	60.3	5961	15	US-10-429-802-35
10	718.8	60.3	5961	16	US-10-430-503-26
11	501.8	42.1	601	15	US-10-267-384-168
12	499.4	41.9	501	16	US-10-411-037-19

RESULT 1
 US-10-284-740-13
 ; Sequence 13, Application US/10284740
 ; Publication No. US20030138404A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Maroun, Leonard E.
 ; TITLE OF INVENTION: INTERFERON RE
 ; DISEASES
 ; FILE REFERENCE: 18448/2002
 ; CURRENT APPLICATION NUMBER: US/10/284,740
 ; CURRENT FILING DATE: 2002-10-31
 ; PRIOR APPLICATION NUMBER: US 09/845,260
 ; PRIOR FILING DATE: 2001-04-30
 ; PRIOR APPLICATION NUMBER: US 09/067,398
 ; PRIOR FILING DATE: 1998-04-28
 ; PRIOR APPLICATION NUMBER: US 08/502,519
 ; PRIOR FILING DATE: 1995-07-14
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 13
 ; LENGTH: 1193
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (109) .. (609)
 ; OTHER INFORMATION:
 ; US-10-284-740-13

Query Match 100.0%; Score 1193; DB 15; Length 1193;
 Best Local Similarity 100.0%; Pred. No. 2.6e-244;
 Matches 1193; Conservative 0; Mismatches 0; Gaps 0;
 Qy 1 TGAAGATCAGCTATTAGAAGAAAGATCAGTTAAGCTTGGACCTGATCGCTGAT 60

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 26, 2004, 10:00:30 ; Search time 31.5556 Seconds
(without alignments)
1887.118 Million cell updates/sec

Title: US-10-655-873-12
Perfect score: 856
Sequence: 1 MKYTSYILLAFLQLCIVLGSIG.....AKTGKRKRSQMLFQGRRASQ 166

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : 2262261 +

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1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMATES

Result No.	Score	Query Match	Length	DB	ID	Description
1	0.9999999999999999	1	1	enwiki	1	enwiki

1	856	100.0	166	1	AAP93414	IFN211	,
2	856	100.0	166	7	ADP76401	Novel hum	
3	856	100.0	166	7	ADM13723	Human int	
4	856	100.0	166	8	ADP12492	Protein e	
5	856	100.0	166	8	ADO19766	Human PRO	
6	856	100.0	166	8	ADQ09094	Human che	
7	852	99.5	166	1	AAP30093	Sequence	
8	852	99.5	166	1	AAP40122	Sequence	
9	852	99.5	166	1	AAP40153	Sequence	
10	852	99.5	166	1	AAP40157	Sequence	
11	852	99.5	166	1	AAP50233	Human rec	
12	852	99.5	166	2	AAW70582	Human int	
13	852	99.5	166	4	AAB99130	Human int	
14	852	99.5	166	5	AAE15823	Human int	
15	852	99.5	166	5	AAU78100	Human int	
16	852	99.5	166	5	AAU98670	Human int	
17	852	99.5	166	5	ABB07440	Abb07440	Interfero
18	852	99.5	166	6	ABR55848	Human int	
19	852	99.5	166	6	ABR40017	Human wil	
20	852	99.5	166	6	ABP56461	ABP56461	Human int
21	852	99.5	166	6	ADA94887	Ada94887	Human int
22	852	99.5	166	7	ADC78909	ADC78909	Human PRO
23	852	99.5	166	8	ADG45031	Adg45031	Human int
24	852	99.5	166	8	ADJ56129	Adj56129	Human int

852	99.5	166	6	ABB56461	Human	int
852	99.5	166	6	ADA94887	Human	int
852	99.5	166	7	ADC78909	Human	PRO
852	99.5	166	8	ADG45031	Human	int
852	99.5	166	8	ADJ56129	Human	int
852	99.5	166	8	ADT56252	Human	int

26	852	99.5	166	8	ADM41333	Human int
27	852	99.5	166	8	ADN02800	Human int
28	852	99.5	166	8	ADN49692	Human int
29	848	99.1	166	1	AAP60250	Modified
30	848	99.1	166	1	AAP99990	Modified
31	847	98.9	166	1	AAP60090	Interfero
32	845	98.7	166	1	AAP50284	Human int
33	844	98.6	166	1	AAP30187	Sequence
34	843	98.5	166	1	AAP40255	Human imm
35	843	98.5	166	1	AAP40043	Sequence
36	842	98.4	166	1	AAP30002	Sequence
37	841	98.2	166	1	AAP40307	Sequence
38	826	96.5	166	1	AAP50170	Sequence
39	755	88.2	146	8	ADL88865	Human cyt
40	755	88.2	147	1	AAP60787	Sequence
41	755	88.2	147	1	AAP81208	Left and
42	755	88.2	177	1	AAP81210	ClaI-BamH
43	751	87.7	146	1	AAP50128	Sequence
44	751	87.7	146	1	GIF146 ga	
45	751	87.7	146	1	AAP60615	
					AAP60344	Human gam

ALIGNMENTS

RESULT 1
AAP93414
ID AAP93414 standard; protein; 166 AA;

AAP93414;
27-APR-1990 (First entry)
IFN211 , IFN-gamma mutant.
Interferon-gamma; mutant; IFN211.
Homo sapiens.

PR	25-APR-1988;	88US-00185219.
XX	(PHIP) PHILLIPS PETROLEUM CO	
PA		
XX		
PI	Thill GP, Davis GR;	
XX		
DR	WPI; 1989-349507/48.	
DR	N-PSDB; AAN92425.	
XX		
PT	Enhanced prodn. of interferon	
PT	<i>Pichia pastoris</i> , transformed	
PT	vector.	

PS Disclosure; Page 7; 26pp; English.
XX CC IFN211 is a mutated form of IFN-gamma structural gene created by deleting
CC the signal sequence by creating an ECO RI site and second start codon at
CC approx. 66, 67, and 68 of the wt sequence. The mutant gene is used to
CC construct IFN-gamma cytoplasmic expression vectors esp. methylotrophic
CC yeast vectors for transformation of *Pichia pastoris*. See also AAP93416
XX sequence 166 22.

```
Query Match          100.0%;  Score 856;  DB 1;  Length 166;  
Best Local Similarity 100.0%;  Pred. No. 2e-77;  
Matches 166;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
```

Db 1 MKYTSYIILAFQLCIVLGLGCYQDPYVKEAENLKKYFNAGHSVDADNGTLEFLGILKNWK 60 CC invention.
 XX SQ Sequence 166 AA;

Qy 61 EESDRKIMOSQIVSPYFKLFLQFKDDQSIQKSVETIKEKDMNVKFNKRRDDFEKLTN 120 Query Match 100.0%; Score 856; DB 7; Length 166;
 Best Local Similarity 100.0%; Pred. No. 2e-77; Mismatches 0; Indels 0; Gaps 0;
 Matches 166; Conservative 0; Sequence 166 AA;

Db 61 EESDRKIMOSQIVSPYFKLFLQFKDDQSIQKSVETIKEKDMNVKFNKRRDDFEKLTN 120 Qy 1 MKYTSYIILAFQLCIVLGLGCYQDPYVKEAENLKKYFNAGHSVDADNGTLEFLGILKNWK 60 Db 1 MKYTSYIILAFQLCIVLGLGCYQDPYVKEAENLKKYFNAGHSVDADNGTLEFLGILKNWK 60

Qy 61 EESDRKIMOSQIVSPYFKLFLQFKDDQSIQKSVETIKEKDMNVKFNKRRDDFEKLTN 120 Qy 1 MKYTSYIILAFQLCIVLGLGCYQDPYVKEAENLKKYFNAGHSVDADNGTLEFLGILKNWK 60 Db 61 EESDRKIMOSQIVSPYFKLFLQFKDDQSIQKSVETIKEKDMNVKFNKRRDDFEKLTN 120

RESULT 2
 ADF76401 1D ADF76401 Standard; protein; 166 AA.
 XX AC ADF76401;
 XX DT 26-FEB-2004 (First entry)
 XX DE Novel human secreted and transmembrane protein SeqID 74.
 XX KW human; PRO; membrane bound protein; membrane bound receptor;
 XX cell proliferation; cell migration; cell differentiation;
 XX mitogenic factor; survival factor; cytotoxic factor;
 XX differentiation factor; neuropeptide; hormone; cell receptor;
 XX receptor-ligand interaction; cytosolic; chondrocyte; tumour;
 XX OS Homo sapiens.
 XX PN WO2003072035-A2.
 XX PD 04-SEP-2003.
 XX PP 21-FEB-2003; 2003WO-US005241.
 XX PR 22-FEB-2002; 2002US-0359461P.
 XX PA (GETH) GENENTECH INC.
 XX PI Bodary SC, Clark H, Hunte B, Jackman JK, Schoenfeld JR;
 XX PI Williams PM, Wood WI, Wu TD;
 XX DR 2003-721702/68.
 XX DR N-PSDB; ADF76400.

PS Claim 10; SEQ ID NO 74; 918pp; English.

XX This invention relates to novel nucleic acids encoding human PRO secreted and transmembrane proteins. Extracellular proteins play important roles in the formation, differentiation and maintenance of multicellular organisms. The fate of many individual cells (for example proliferation, migration or differentiation) is typically governed by information received from other cells and the immediate environment. The information is often transmitted by secreted polypeptides (for example mitogenic factors, survival factors, cytotoxic factors, differentiation factors, neuropeptides and hormones) which are received and interpreted by diverse cell receptors or membrane bound proteins. These membrane bound proteins and receptors may be of use as pharmaceutical and diagnostic agents, such as in the blocking of receptor-ligand interactions. The current invention provides the amino acid sequences of novel human membrane bound receptors and proteins, along with the cDNA sequences encoding them. The novel proteins of the invention may have cytostatic activities through the stimulation of chondrocytes. The nucleic acids of the invention may be useful for the manufacture of a medicament for diagnosing or treating a tumour in a mammal. In addition, they may be useful for measuring or detecting the expression of a tumour associated gene. The present sequence is the amino acid sequence of a human PRO protein of the

XX CC invention provides composition for preventing or decreasing CC pathological effects of a disease that are associated with an increased CC level of or a heightened responsiveness to interferon (IFN) where the CC composition inhibits the activity of one or more IFN. The invention is CC useful for treating diseases such as Alzheimer's disease, Down syndrome, CC infant encephalitis, ulcerative colitis, Hashimoto's disease such as lupus erythematosus, CC autoimmunity diseases such as amyotrophic lateral sclerosis, CC and Goodpasture's syndrome and HIV where the administration of the CC antagonist prevents or ameliorates AIDS (acquired immunodeficiency

XX Disclosure; Fig 7B; 38pp; English.

XX The present invention provides composition for preventing or decreasing CC pathological effects of a disease that are associated with an increased CC level of or a heightened responsiveness to interferon (IFN) where the CC composition inhibits the activity of one or more IFN. The invention is CC useful for treating diseases such as Alzheimer's disease, Down syndrome, CC infant encephalitis, ulcerative colitis, Hashimoto's disease such as lupus erythematosus, CC autoimmunity diseases such as amyotrophic lateral sclerosis, CC and Goodpasture's syndrome and HIV where the administration of the CC antagonist prevents or ameliorates AIDS (acquired immunodeficiency